EXHIBIT A

Summary Of Nogo Hydrophilicity Analysis

Tax No of Exhibit B	Amino Acid Sequence of Interest ("I")	Claim	Analyzed Amino Acid Sequence ("A")	Amino Acid positions of I in A	Point Of Greatest Local Hydrophilicity
1	amino acids 1-171 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-171 in the blot corresponding to aa 1-171 of SEQ ID NO:2	ca. aa 42
2	amino acids 172-974 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-803 in the blot corresponding to aa 172-974 of SEQ ID NO:2	Peaks throughout the protein
3	amino acids 542-722 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-181 in the blot corresponding to aa 542-722 of SEQ ID NO:2	ca. aa 114
4	amino acids 172-723 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-552 in the blot corresponding to aa 172-723 of SEQ ID NO:2	ca. aa 145
5	amino acids 1-974 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-974 in the blot corresponding to aa 1-974 of SEQ ID NO:2	Peaks throughout the protein
6	amino acids 1-131 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-131 in the blot corresponding to aa 1-131 of SEQ ID NO:29	ca. aa 40

Tax No of Exhibit B	Amino Acid Sequence of Interest ("I")	Claim	Analyzed Amino Acid Sequence ("A")	Amino Acid positions of I in A	Point Of Greatest Local Hydrophilicity
7	amino acids 132-939 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-808 in the blot corresponding to aa 132-939 of SEQ ID NO:29	Peaks throughout the protein
8	amino acids 206-501 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-296 in the blot corresponding to aa 206-501 of SEQ ID NO:29	ca. aa 112
9	amino acids 501-680 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-180 in the blot corresponding to aa 501-680 of SEQ ID NO:29	ca. aa 162
10	amino acids 132-206 of SEQ ID NO:29	Claim 136 & 137	aa 100-300 of SEQ ID NO:29	aa 32-106 in the blot corresponding to aa 132-206 of SEQ ID NO:29	ca. aa 36
11	amino acids 680-939 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-260 in the blot corresponding to aa 680-939 of SEQ ID NO:29	Peaks throughout the protein
12	amino acids 940-1127 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-188 in the blot corresponding to aa 940-1127 of SEQ ID NO:29	ca. aa 23 and aa 32
13	amino acids 623-640 of SEQ ID NO:2	Claim 135	aa 550-750 of SEQ ID NO:2	aa 73-90 in the blot corresponding to aa 623-640 of SEQ ID NO:2	ca. 80

Tax No of Exhibit B	Amino Acid Sequence of Interest ("I")	Claim	Analyzed Amino Acid Sequence ("A")	Amino Acid positions of I in A	Point Of Greatest Local Hydrophilicity
14	SEQ ID NO:43	Claim 135	aa 1-200 of SEQ ID NO. 29	aa 1-13 in the blot corresponding to aa 1-13 of SEQ ID NO. 29	ca. 10
15	SEQ ID NO:44	Claim 135	aa 100-300 of SEQ ID NO. 29	aa 88-104 in the blot corresponding to aa 187-203 of SEQ ID NO. 29	ca. 95
16	SEQ ID NO:45	Claim 135	aa 250-450 of SEQ ID NO. 29	aa 91-111 in the blot corresponding to aa 570-619 of SEQ ID NO. 29	ca. 105
17	SEQ ID NO:46	Claim 135	entire sequence of interest	aa 1-50	21
18	Amino acids 762-1163 of SEQ ID NO:2	Claim 135	Entire sequence of interest	aa 1-402	ca. 195

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 MEDIDQSSLV SSSTDSPPRP PPAFKYQFVT EPEDEEDEEE EEDEEEDDED LEELEVLERK    60
   61 PAAGLSAAAV PPAAAAPLLD FSSDSVPPAP RGPLPAAPPA APERQPSWER SPAAPAPSLP   120
  121 PAAAVLPSKL PEDDEPPARP PPPPPAGASP LAEPAAPPST PAAPKRRGSG S

SEQUENCE LENGTH: 171
```

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

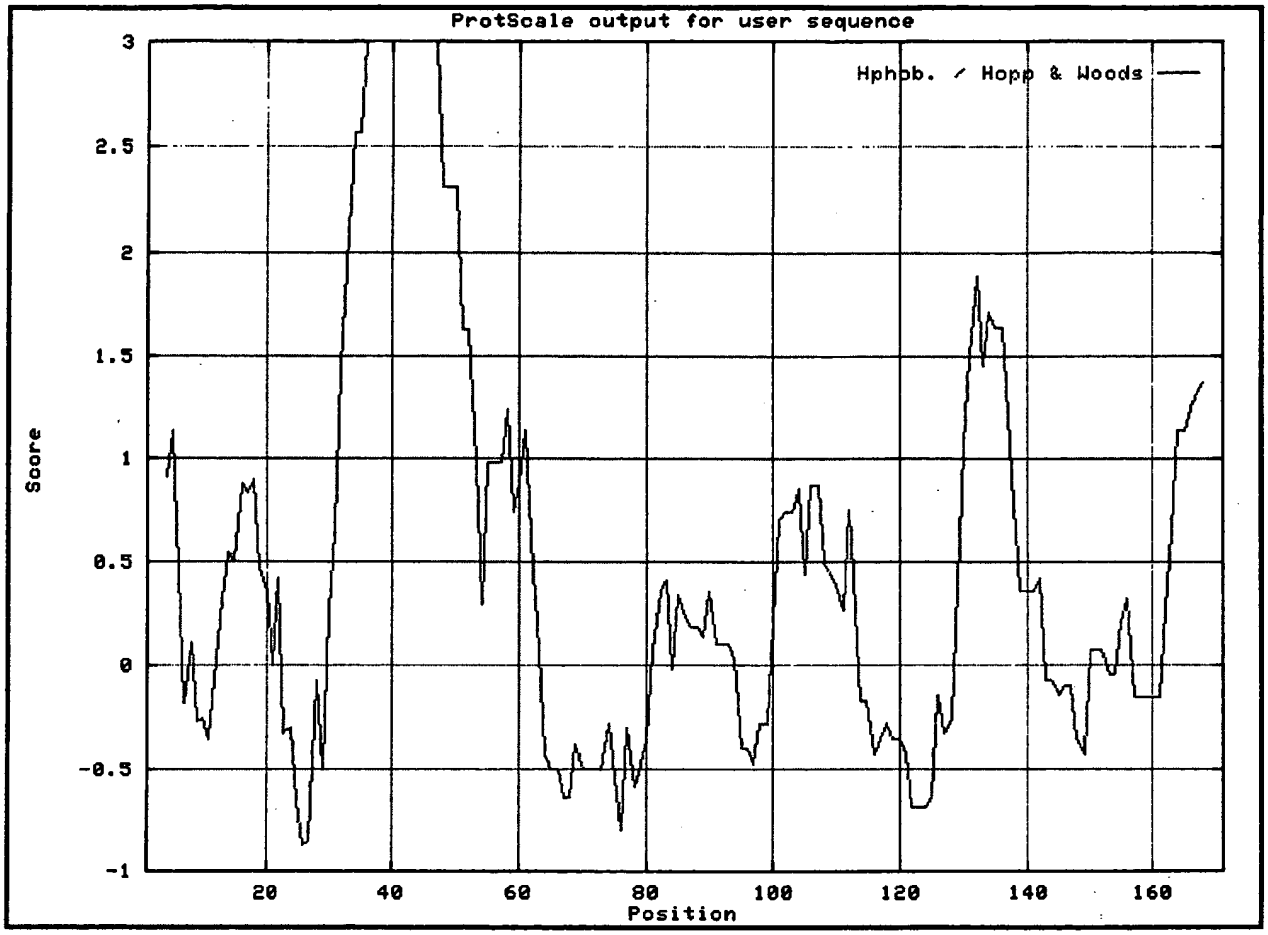
```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
   1     2     3     4     5     6     7
1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge              center              edge
```

```
MIN: -0.871
MAX: 3.000
```

1-171 of SEQ ID NO 2 (claim 13) (15)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 VDETLFALPA ASEPVIPSSA EKIMDLMEQP GNTVSSGQED FPSVLLETAA SLPSLSPLST    60
   61 VSFKEHGYLG NLSAVSSSEG TIEETLNEAS KELPERATNP FVNRDLAEFS ELEYSEMGSS   120
  121 FKGSPKGESA ILVENTKEEV IVRSKDKEDL VCSAALHSPQ ESPVGKEDRV VSPEKTMDIF   180
  181 NEMQMSVVAP VREEYADFKP FEQAWEVKDT YEGSRDVLAA RANVESKVDR KCLEDSLEQK   240
  241 SLGKDSEGRN EDASFPSTPE PVKDSSRAYI TCASFTSATE STTANTFPLL EDHTSENKTD   300
  301 EKKIEERKAQ IITEKTSPKT SNPFLVAVQD SEADYVTTDT LSKVTEAAVS NMPEGLTPDL   360
  361 VQEACESELN EATGTKIAYE TKVDLVQTSE AIQESLYPTA QLCPSFEEAE ATPSPVLPDI   420
  421 VMEAPLNSLL PSAGASVVQP SVSPLEAPPP VSYDSIKLEP ENPPPYEEAM NVALKALGTK   480
  481 EGIKEPESFN AAVQETEAPY ISIACDLIKE TKLSTEPSPD FSNYSEIAKF EKSVPEHAEL   540
  541 VEDSSPESEP VDLFSDDSIP EVPQTQEEAV MLMKESLTEV SETVAQHKEE RLSASPQELG   600
  601 KPYLESFQPN LHSTKDAASN DIPTLTKKEK ISLQMEEFNT AIYSNDDLLS SKEDKIKESE   660
  661 TFSDSSPIEI IDEFPTFVSA KDDSPKLAKE YTDLEVSDKS EIANIQSGAD SLPCLELPCD   720
  721 LSFKNIYPKD EVHVSDEFSE NRSSVSKASI SPSNVSALEP QTEMGSIVKS KSLTKEAEKK   780
  781 LPSDTEKEDR SLSAVLSAEL SKT
```

SEQUENCE LENGTH: 803

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

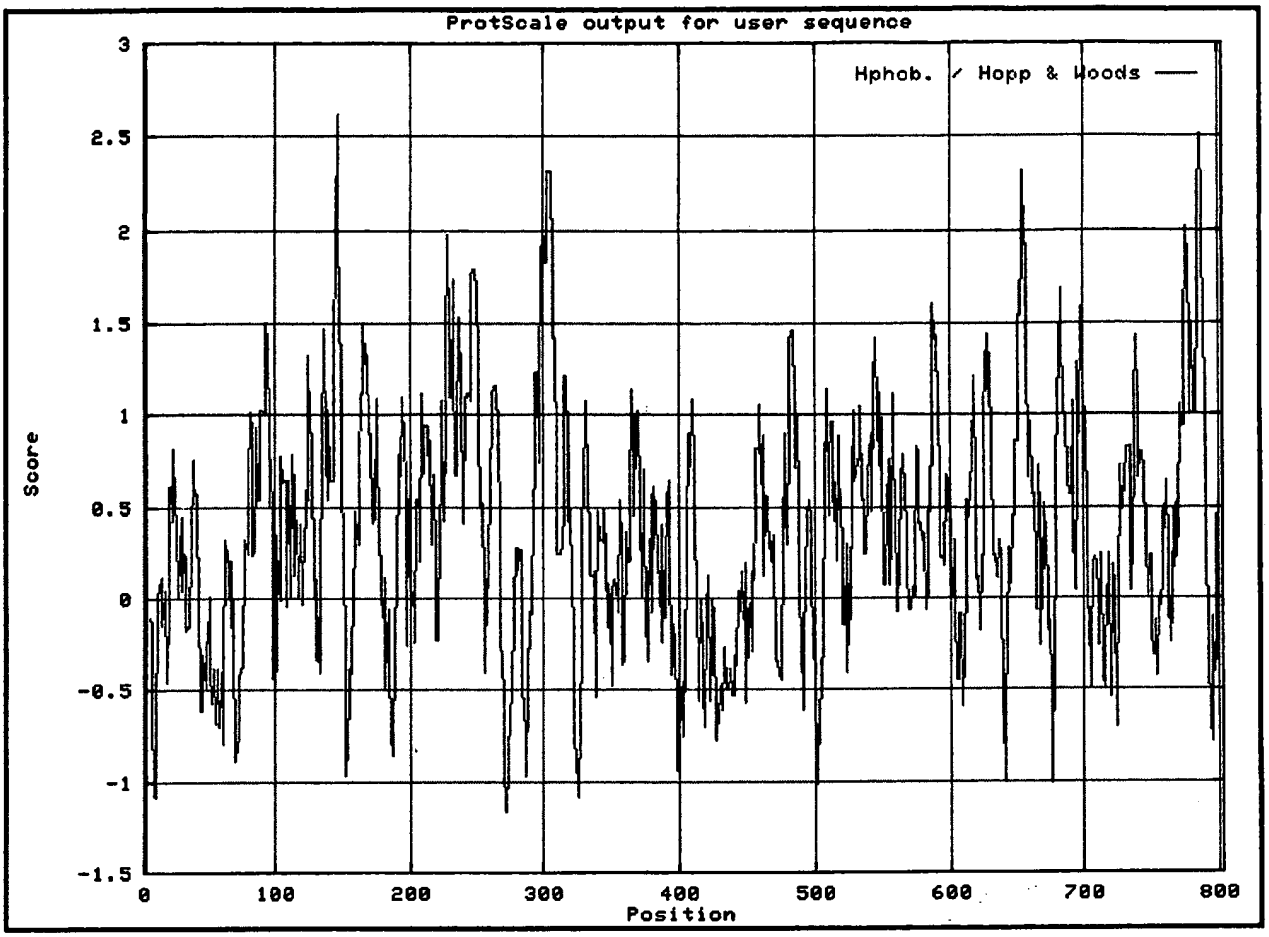
Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

Weights for window positions 1,..,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.171
MAX: 2.614

172-974 of SEQ ID NO: 2 (claim 13) (16)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page **Site Map** **Search ExPASy** **Contact us** **Swiss-Prot** **Proteomics tools**

ExPASy Home page **Site Map** **Search ExPASy** **Contact us** **Swiss-Prot** **Proteomics tools**

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 EATGTKIAYE TKVDLVQTSE AIQESLYPTA QLCPSFEEAE ATPSPVLPDI VMEAPLNSLL    60
   61 PSAGASVVQP SVSPLEAPPP VSYDSIKLEP ENPPPYEEAM NVALKALGTK EGIKEPESFN   120
  121 AAVQETEAPY ISIACDLIKE TKLSTEPSPD FSNYSEIAKF EKSVPEHAEL VEDSSPESEP   180
  181 V
```

SEQUENCE LENGTH: 181

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

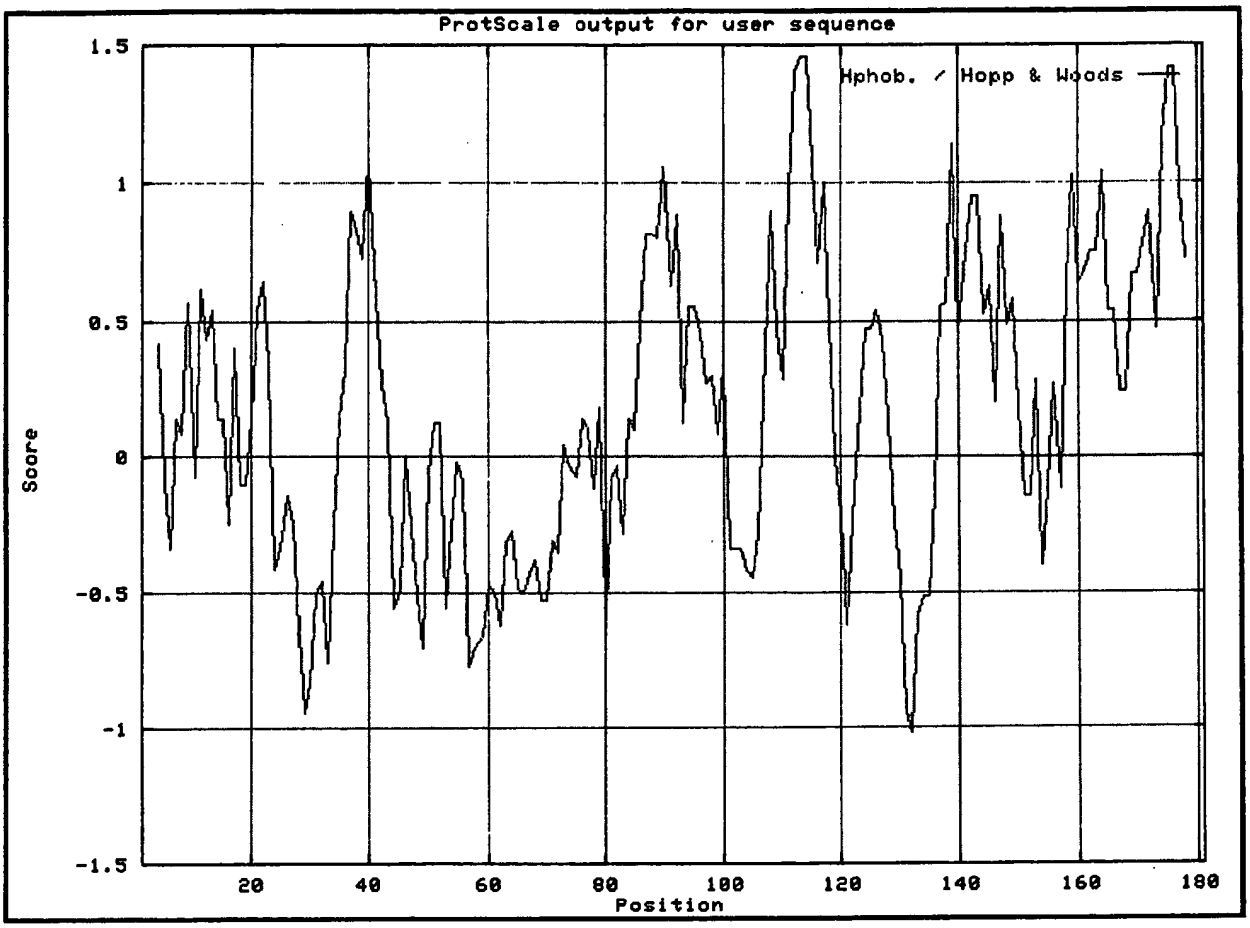
```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
  1     2     3     4     5     6     7
1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge              center              edge
```

MIN: -1.014
MAX: 1.457

542-722 of
SEQ ID No. 2
(claim 13) (18)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 VDETLFALPA ASEPVIPSSA EKIMDLMEQP GNTVSSGQED FPSVLLETAA SLPSLSPLST    60
   61 VSFKEHGYLG NLSAVSSSEG TIEETLNEAS KELPERATNP FVNRDLAEFS ELEYSEMGSS   120
  121 FKGSPKGESA ILVENTKEEV IVRSKDKEDL VCSAALHSPQ ESPVGKEDRV VSPEKTMDIF   180
  181 NEMQMSVVAP VREEYADFKP FEQAWEVKDT YEGSRDVLAA RANVESKVDR KCLEDSLEQK   240
  241 SLGKDSEGRN EDASFPSTPE PVKDSSRAYI TCASFTSATE STTANTFPLL EDHTSENKTD   300
  301 EKKIEERKAQ IITEKTSPKT SNPFLVAVQD SEADYVTTDT LSKVTEAAVS NMPEGLTPDL   360
  361 VQEACESELN EATGTKIAYE TKVDLVQTSE AIQESLYPTA QLCPSFEEAE ATPSPVLPDI   420
  421 VMEAPLNSLL PSAGASVVQP SVSPLEAPPP VSYDSIKLEP ENPPPYEEAM NVALKALGTK   480
  481 EGIKEPESFN AAVQETEAPY ISIACDLIKE TKLSTEPSPD FSNYSEIAKF EKSVPEHAEL   540
  541 VEDSSPESEP VD
```

SEQUENCE LENGTH: 552

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

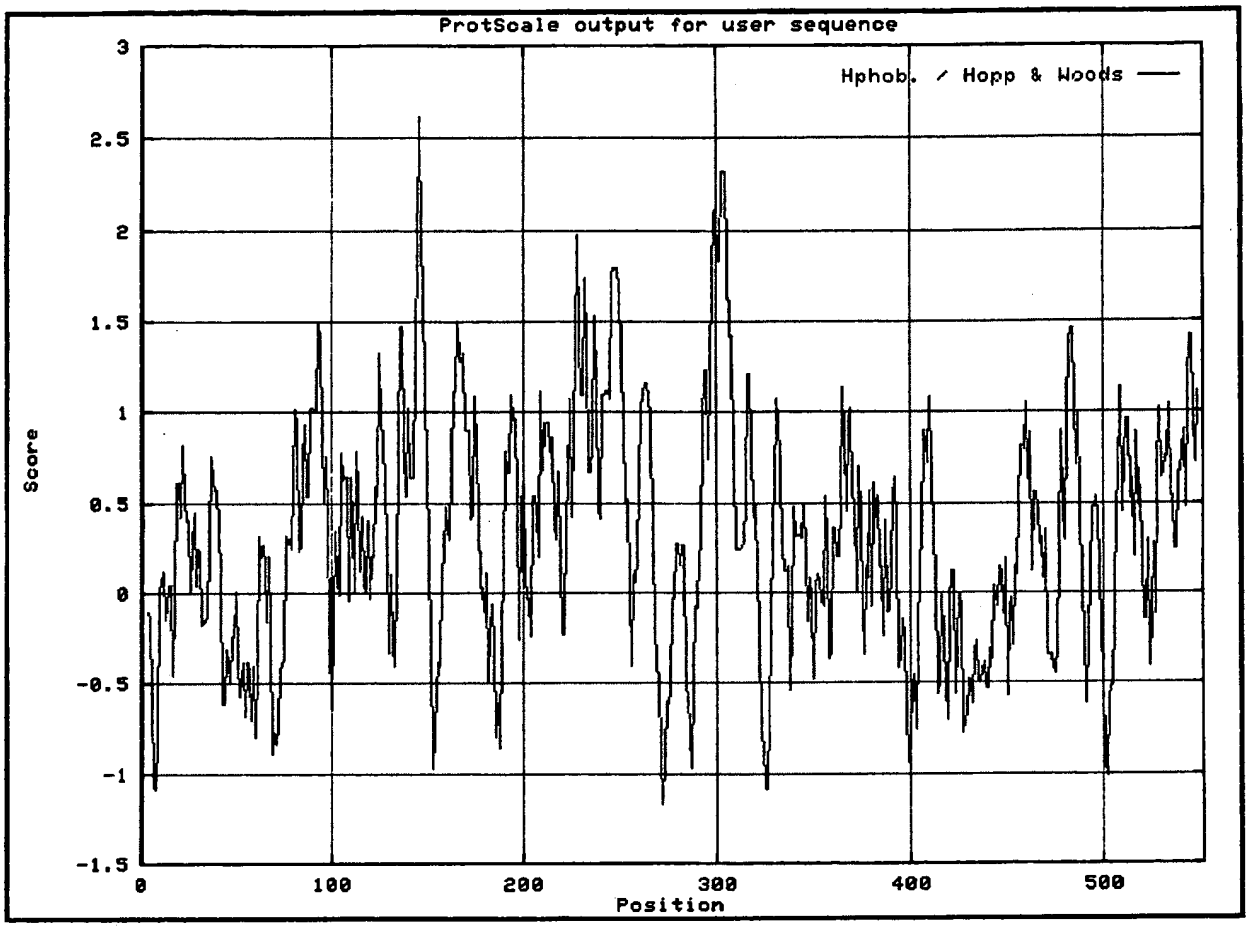
Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

Weights for window positions 1,..,7, using **linear weight variation model:**

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.171
MAX: 2.614

172-723 of SEQ ID NO 2 (Claim 13) (21)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 MEDIDQSSLV SSSTDSPPRP PPAFKYQFVT EPEDEEDEEE EEDEEEDDED LEELEVLERK    60
   61 PAAGLSAAAV PPAAAAPLLD FSSDSVPPAP RGPLPAAPPA APERQPSWER SPAAPAPSLP   120
  121 PAAAVLPSKL PEDDEPPARP PPPPPAGASP LAEPAAPPST PAAPKRRGSG SVDETLFALP   180
  181 AASEPVIPSS AEKIMDLMEQ PGNTVSSGQE DFPSVLLETA ASLPSLSPLS TVSFKEHGYL   240
  241 GNLSAVSSSE GTIEETLNEA SKELPERATN PFVNRDLAEF SELEYSEMGS SFKGSPKGES   300
  301 AILVENTKEE VIVRSKDKED LVCSAALHSP QESPVGKEDR VVSPEKTMDI FNEMQMSVVA   360
  361 PVREEYADFK PFEQAWEVKD TYEGSRDVLA ARANVESKVD RKCLEDSLEQ KSLGKDSEGR   420
  421 NEDASFPSTP EPVKDSSRAY ITCASFTSAT ESTTANTFPL LEDHTSENKT DEKKIEERKA   480
  481 QIITEKTSPK TSNPFLVAVQ DSEADYVTTD TLSKVTEAAV SNMPEGLTPD LVQEACESEL   540
  541 NEATGTKIAY ETKVDLVQTS EAIQESLYPT AQLCPSFEEA EATPSPVLPD IVMEAPLNSL   600
  601 LPSAGASVVQ PSVSPLEAPP PVSYDSIKLE PENPPPYEEA MNVALKALGT KEGIKEPESF   660
  661 NAAVQETEAP YISIACDLIK ETKLSTEPSP DFSNYSEIAK FEKSVPEHAE LVEDSSPESE   720
  721 PVDLFSDDSI PEVPQTQEEA VMLMKESLTE VSETVAQHKE ERLSASPQEL GKPYLESFQP   780
  781 NLHSTKDAAS NDIPTLTKKE KISLQMEEFN TAIYSNDDLL SSKEDKIKES ETFSDSSPIE   840
  841 IIDEFPTFVS AKDDSPKLAK EYTDLEVSDK SEIANIQSGA DSLPCLELPC DLSFKNIYPK   900
  901 DEVHVSDEFS ENRSSVSKAS ISPSNVSALE PQTEMGSIVK SKSLTKEAEK KLPSDTEKED   960
  961 RSLSAVLSAE LSKT
```

SEQUENCE LENGTH: 974

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

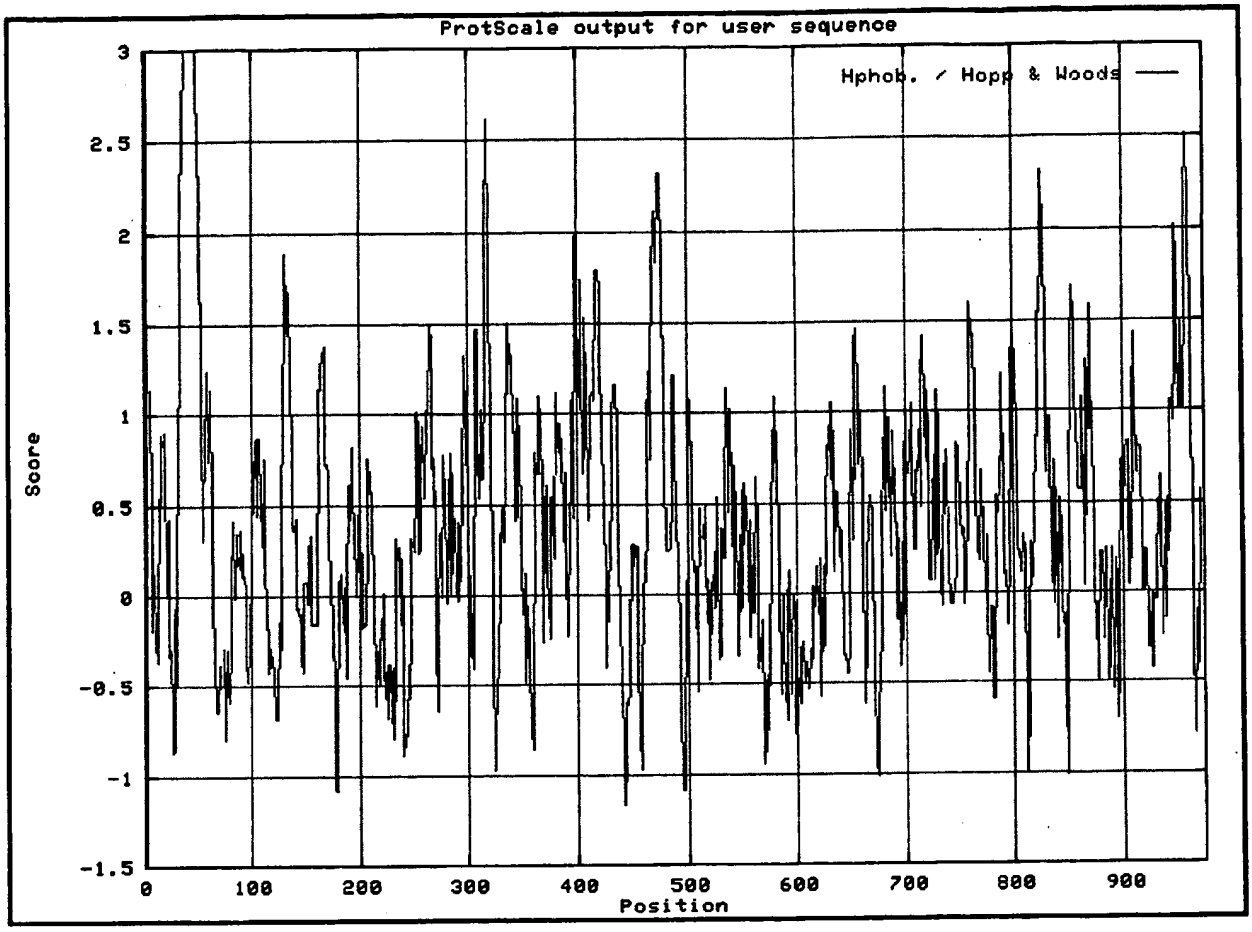
Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

Weights for window positions 1,..,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.171
MAX: 3.000

1-974 of SEQ ID No 2 (Claim 13) (22)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 MEDLDQSPLV SSSDSPPRPQ PAFKYQFVRE PEDEEEEEEE EEEDEDEDLE ELEVLERKPA    60
   61 AGLSAAPVPT APAAGAPLMD FGNDFVPPAP RGPLPAAPPV APERQPSWDP SPVSSTVPAP   120
  121 SPLSAAAVSP S
```

SEQUENCE LENGTH: 131

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

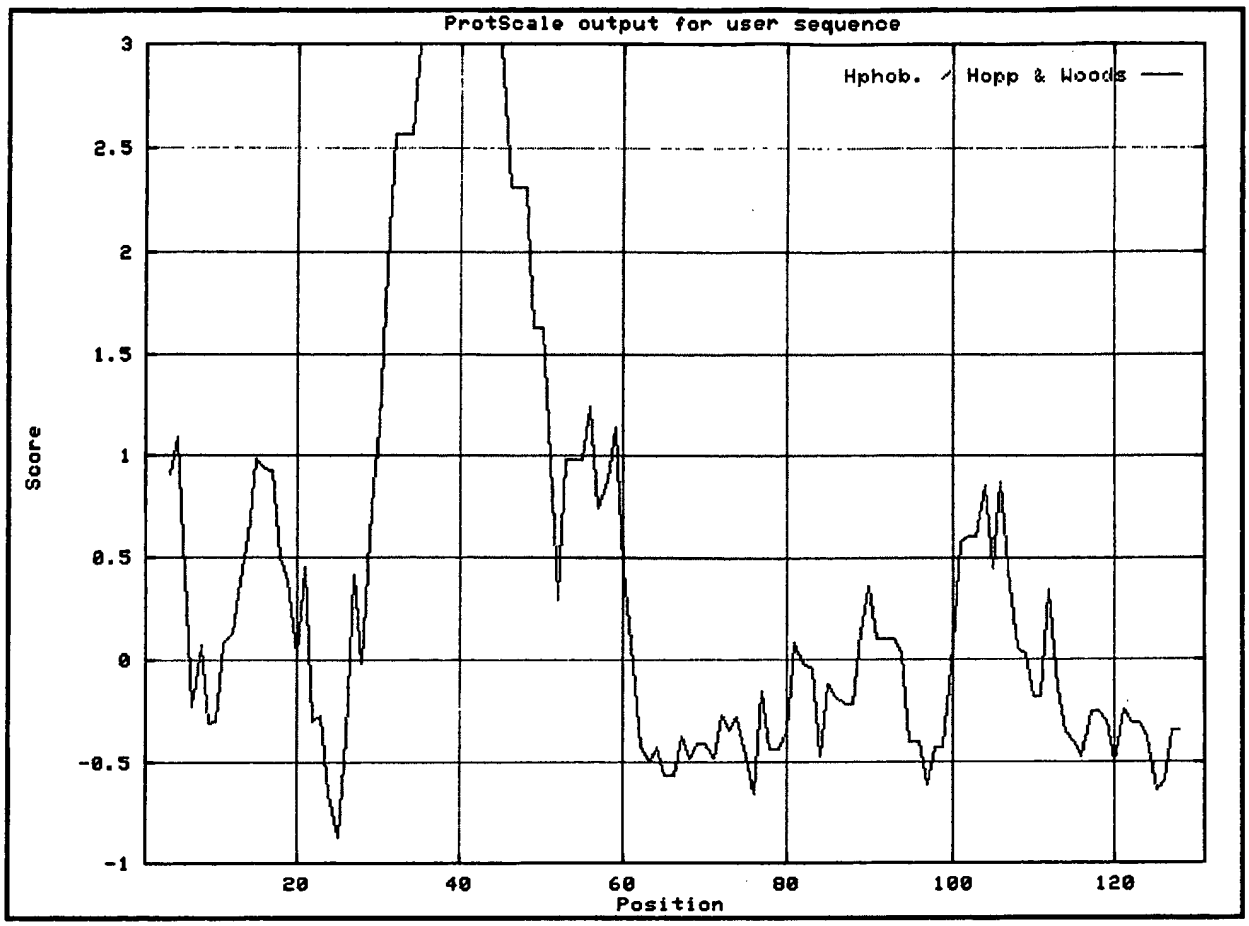
```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
   1     2     3     4     5     6     7
1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge              center              edge
```

```
MIN: -0.871
MAX: 3.000
```

1-131 of
SEQ ID No. 29
(claim 13) (24)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 KLPEDDEPPA RPPPPPPASV SPQAEPVWTP PAPAPAAPPS TPAAPKRRGS SGAVVXXXXK    60
   61 IMDLKEQPGN TISAGQEDFP SVLLETAASX PSLSPLSAAS FKEHEYLGNL STVLPTEGTL   120
  121 QENVSEASKE VSEKAKTLLI DRDLTEFSEL EYSEMGSSFS VSPKAESAVI VANPREEIIV   180
  181 KNKDEEEKLV SNNILHXQQE LPTALTKLVK EDEVVSSEKA KDSFNEKRVA VEAPMREEYA   240
  241 DFKPFERVWE VKDSKEDSDM LAAGGKIESN LESKVDKKCF ADSLEQTNHE KDSESSNDDT   300
  301 SFPSTPEGIK DRSGAYITCA PFNPAATESI ATNIFPLLED PTSENXTDEK KIEEKKAQIV   360
  361 TEKNTSTKTS NPFFVAAQDS ETDYVTTDNL TKVTEEVVAN MPEGLTPDLV QEACESELNE   420
  421 VTGTKIAYET KMDLVQTSEV MQESLYPAAQ LCPSFEESEA TPSPVLPDIV MEAPLNSAVP   480
  481 SAGASVIQPS SSPLEASSVN YESIKHEPEN PPPYEEAMSV SLKVSGIKEE IKEPENINAA   540
  541 LQETEAPYIS IACDLIKETK LSAEPAPDFS DYSEMAKVEQ PVPDHSELVE DSSPDSEPVD   600
  601 LFSDDSIPDV PQKQDETVML VKESLTETSF ESMIEYENKE KLSALPPEGG KPYLESFKLS   660
  661 LDNTKDTLLP DEVSTLSKKE KIPLQMEELS TAVYSNDDLF ISKEAQIRET ETFSDSSPIE   720
  721 IIDEFPTLIS SKTDSFSKLA REYTDLEVSH KSEIANAPDG AGSLPCTELP HDLSLKNIQP   780
  781 KVEEKISFSD DFSKNGSATS KVLLLPPD
```

SEQUENCE LENGTH: 808

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

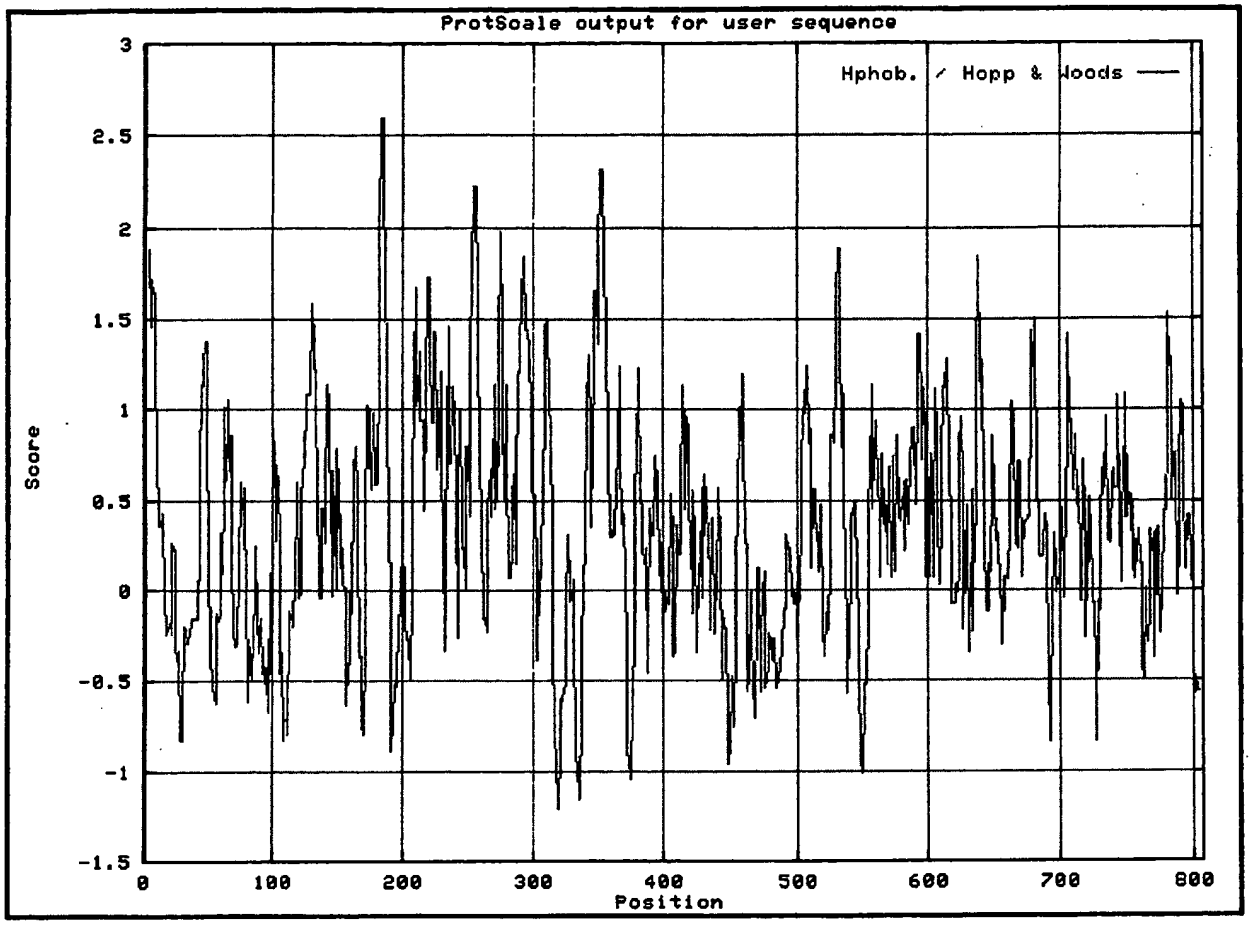
Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

Weights for window positions 1,..,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.214
MAX: 2.600

132-939 of SEQ ID No. 29 (claim 23) (25)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 GQEDFPSVLL ETAASXPSLS PLSAASFKEH EYLGNLSTVL PTEGTLQENV SEASKEVSEK    60
   61 AKTLLIDRDL TEFSELEYSE MGSSFSVSPK AESAVIVANP REEIIVKNKD EEEKLVSNNI   120
  121 LHXQQELPTA LTKLVKEDEV VSSEKAKDSF NEKRVAVEAP MREEYADFKP FERVWEVKDS   180
  181 KEDSDMLAAG GKIESNLESK VDKKCFADSL EQTNHEKDSE SSNDDTSFPS TPEGIKDRSG   240
  241 AYITCAPFNP AATESIATNI FPLLEDPTSE NXTDEKKIEE KKAQIVTEKN TSTKTS
```

SEQUENCE LENGTH: 296

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

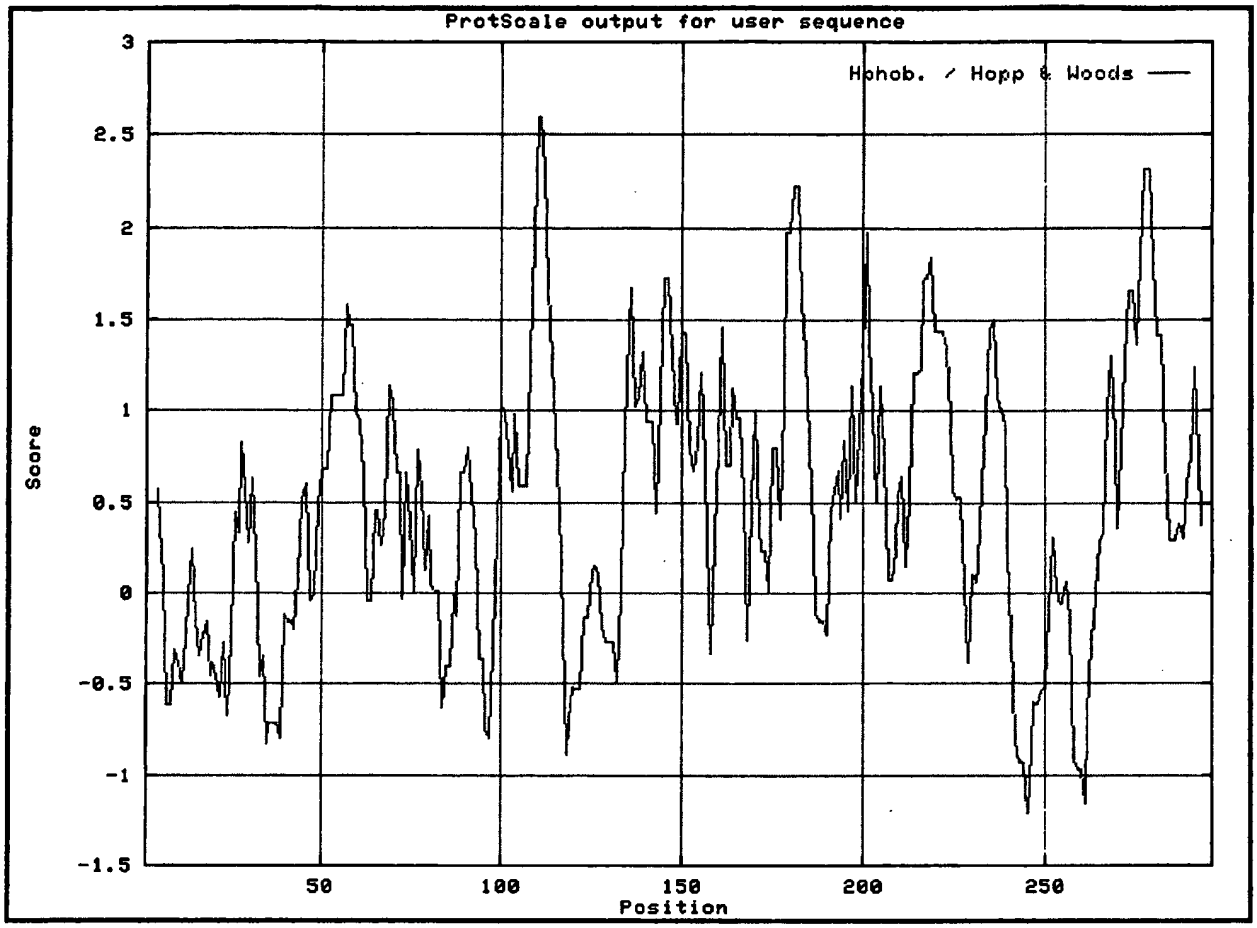
```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
  1     2     3     4     5     6     7
1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge              center              edge
```

MIN: -1.214
MAX: 2.600

206-501 of SEQ ID NO 29 (claim 13) (26)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 SNPFFVAAQD SETDYVTTDN LTKVTEEVVA NMPEGLTPDL VQEACESELN EVTGTKIAYE    60
   61 TKMDLVQTSE VMQESLYPAA QLCPSFEESE ATPSPVLPDI VMEAPLNSAV PSAGASVIQP   120
  121 SSSPLEASSV NYESIKHEPE NPPPYEEAMS VSLKVSGIKE EIKEPENINA ALQETEAPYI

SEQUENCE LENGTH: 180
```

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

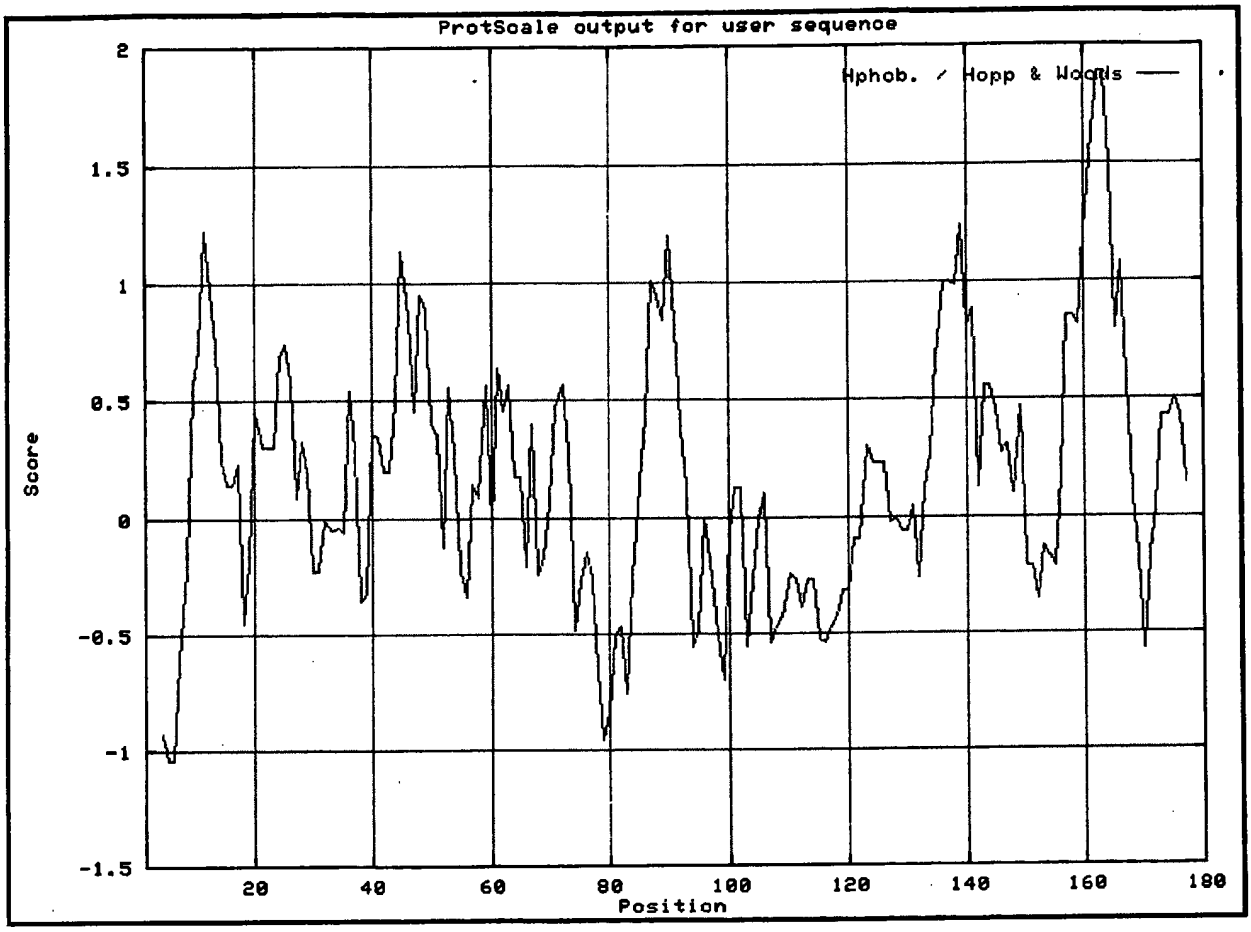
```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
  1     2     3     4     5     6     7
1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge              center              edge
```

```
MIN: -1.043
MAX: 1.886
```

501—680 of SEQ ID NO 29 (claim 1) (27)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 VAPERQPSWD PSPVSSTVPA PSPLSAAAVS PSKLPEDDEP PARPPPPPPA SVSPQAEPVW    60
   61 TPPAPAPAAP PSTPAAPKRR GSSGAVVXXX XKIMDLKEQP GNTISAGQED FPSVLLETAA   120
  121 SXPSLSPLSA ASFKEHEYLG NLSTVLPTEG TLQENVSEAS KEVSEKAKTL LIDRDLTEFS   180
  181 ELEYSEMGSS FSVSPKAESA V
```

SEQUENCE LENGTH: 201

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

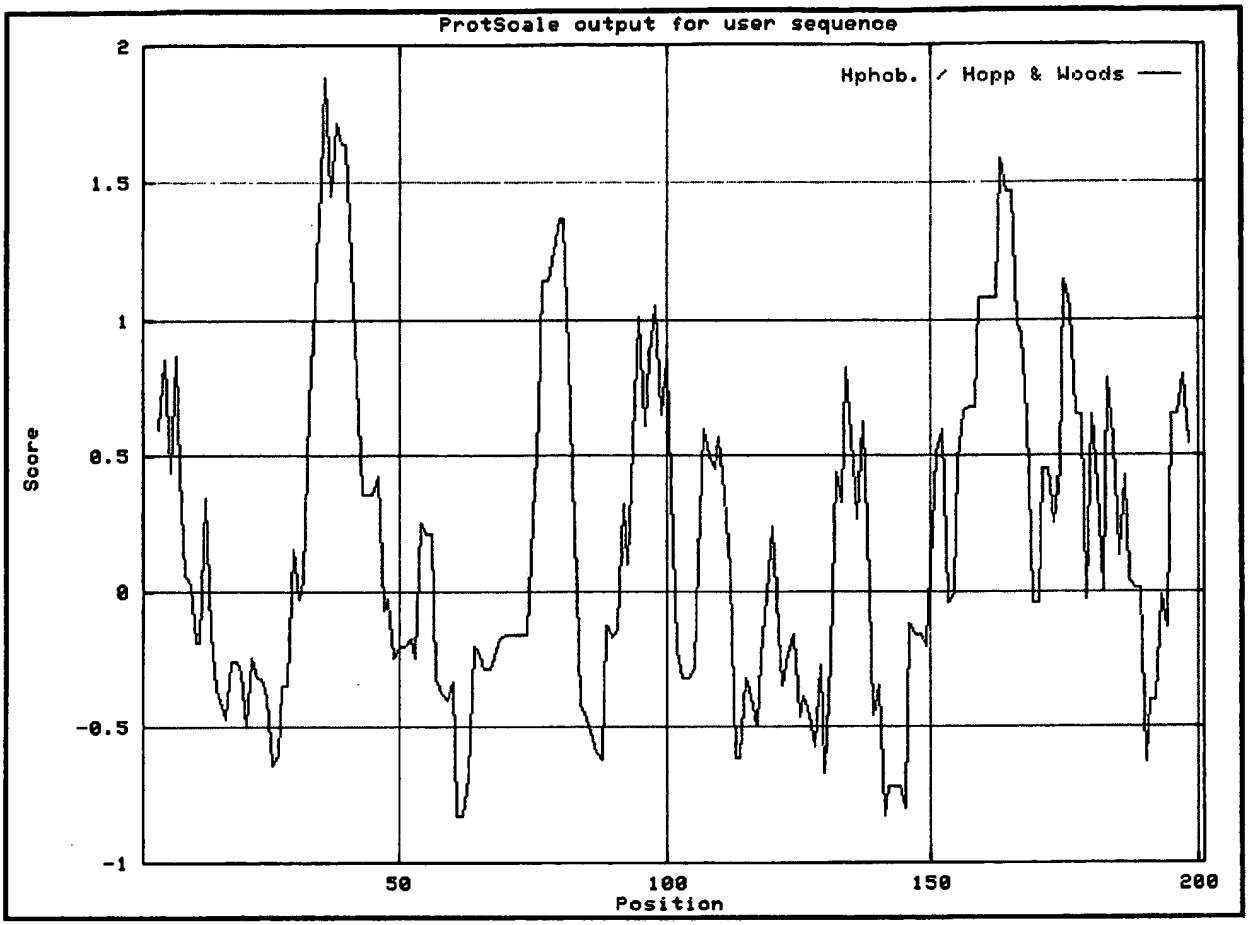
```
  1     2     3     4     5     6     7
1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge              center              edge
```

MIN: -0.829
MAX: 1.886

100-300 of SEQ ID No 29 (Claim 13)

132-206 (32-106)

(28)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 ISIACDLIKE TKLSAEPAPD FSDYSEMAKV EQPVPDHSEL VEDSSPDSEP VDLFSDDSIP    60
   61 DVPQKQDETV MLVKESLTET SFESMIEYEN KEKLSALPPE GGKPYLESFK LSLDNTKDTL   120
  121 LPDEVSTLSK KEKIPLQMEE LSTAVYSNDD LFISKEAQIR ETETFSDSSP IEIIDEFPTL   180
  181 ISSKTDSFSK LAREYTDLEV SHKSEIANAP DGAGSLPCTE LPHDLSLKNI QPKVEEKISF   240
  241 SDDFSKNGSA TSKVLLLPPD
```

SEQUENCE LENGTH: 260

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

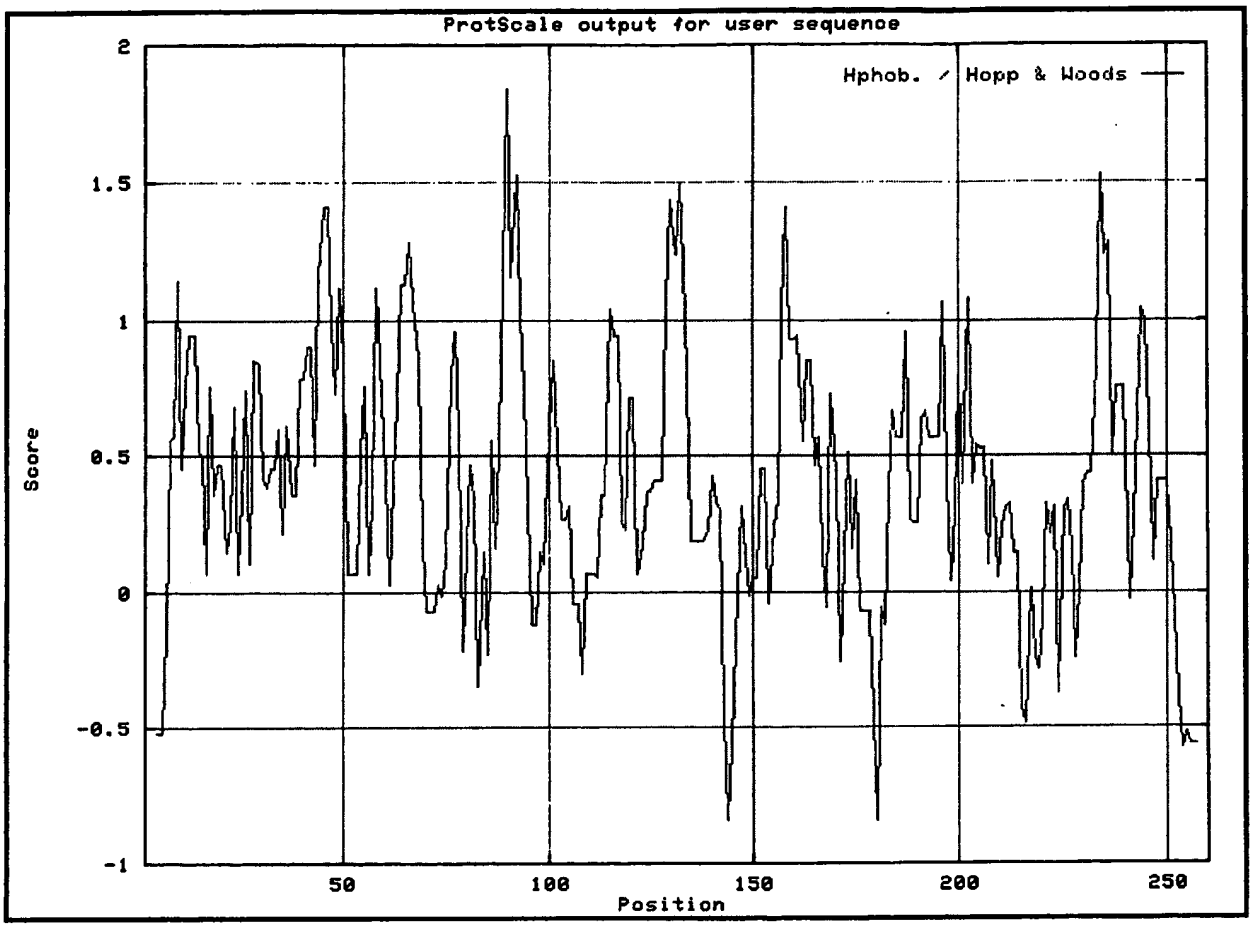
```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
  1     2     3     4     5     6     7
1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge              center              edge
```

```
MIN: -0.843
MAX: 1.843
```

680-939 of
SEQ ID No. 29
(Claim 13)(29)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 VSALGHTQAE IESIVKPKVL EKEAEKKLPS DTEKEDRSPS AIFSADLGKT SVVDLLYWRD    60
   61 IKKTGVVFGA SLFLLLSLTV FSIVSVTAYI ALALLSVTIS FRIYKGVIQA IQKSDEGHPF   120
  121 RAYLESEVAI SEELVQKYSN SALGHVNCTI KELRRLFLVD DLVDSLKFAV LMWVFTYVGA   180
  181 LFNGLTLL
```

SEQUENCE LENGTH: 188

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

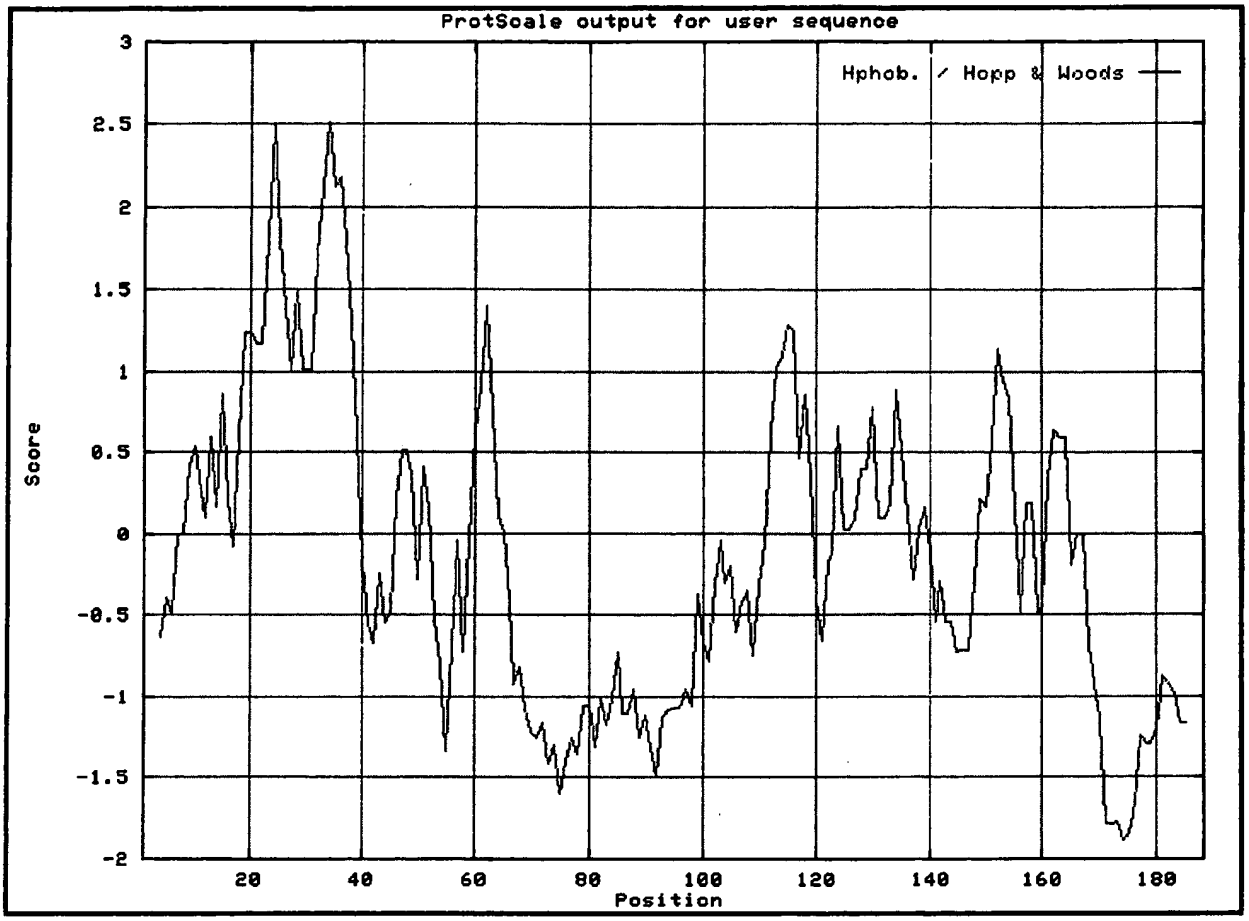
Ala:	-0.500	Arg:	3.000	Asn:	0.200	Asp:	3.000	Cys:	-1.000	Gln:	0.200
Glu:	3.000	Gly:	0.000	His:	-0.500	Ile:	-1.800	Leu:	-1.800	Lys:	3.000
Met:	-1.300	Phe:	-2.500	Pro:	0.000	Ser:	0.300	Thr:	-0.400	Trp:	-3.400
Tyr:	-2.300	Val:	-1.500	Asx:	1.600	Glx:	1.600	Xaa:	-0.215		

Weights for window positions 1,..,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.886
MAX: 2.514

940-1127 of SEQ ID No 29 (Claim 13) (33)



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
      1          11         21         31         41         51
      |          |          |          |          |          |
    1 YETKVDLVQT SEAIQESLYP TAQLCPSFEE AEATPSPVLP DIVMEAPLNS LLPSAGASVV    60
   61 QPSVSPLEAP PPVSYDSIKL EPENPPPYEE AMNVALKALG TKEGIKEPES FNAAVQETEA   120
  121 PYISIACDLI KETKLSTEPS PDFSNYSEIA KFEKSVPEHA ELVEDSSPES EPVDLFSDDS   180
  181 IPEVPQTQEE AVMLMKESLT E

SEQUENCE LENGTH: 201
```

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

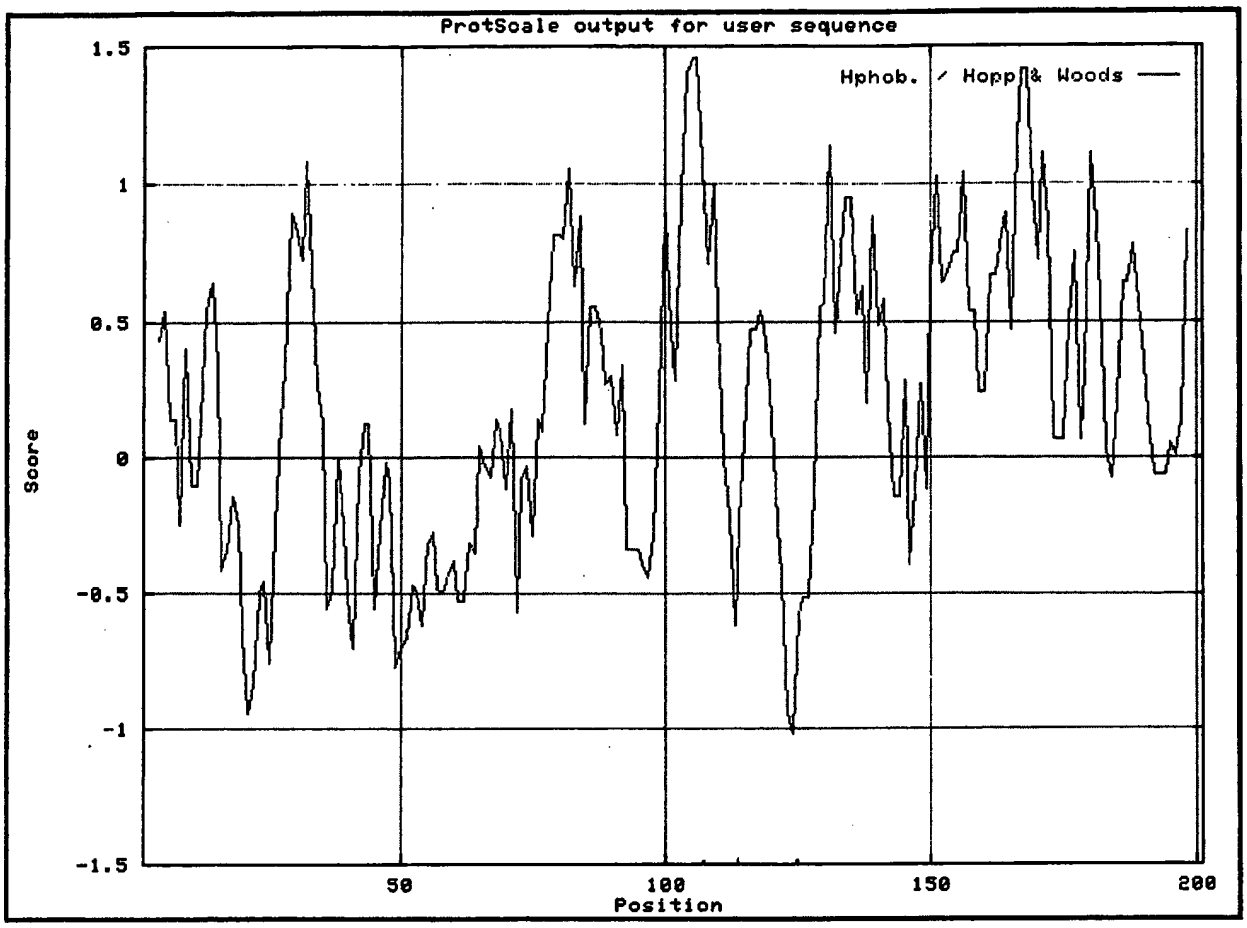
```
  1     2     3     4     5     6     7
1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge              center              edge
```

```
MIN: -1.014
MAX: 1.457
```

Claim 18
550-750 of
Seq ID No. 2

623-640
(73-90)

35



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot Proteomics tools

Search Swiss-Prot/TrEMBL for Go Clear

ProtScale

User-provided sequence:

```
        10         20         30         40         50         60
MEDLDQSPLV SSSDSPPRPQ PAFKYQFVRE PEDEEEEEEE EEEDEDEDLE ELEVLERKPA
        70         80         90        100        110        120
AGLSAAPVPT APAAGAPLMD FGNDFVPPAP RGPLPAAPPV APERQPSWDP SPVSSTVPAP
       130        140        150        160        170        180
SPLSAAAVSP SKLPEDDEPP ARPPPPPPAS VSPQAEPVWT PPAPAPAAPP STPAAPKRRG
       190        200
SSGAVVXXXX KIMDLKEQPG
```

SEQUENCE LENGTH: 200

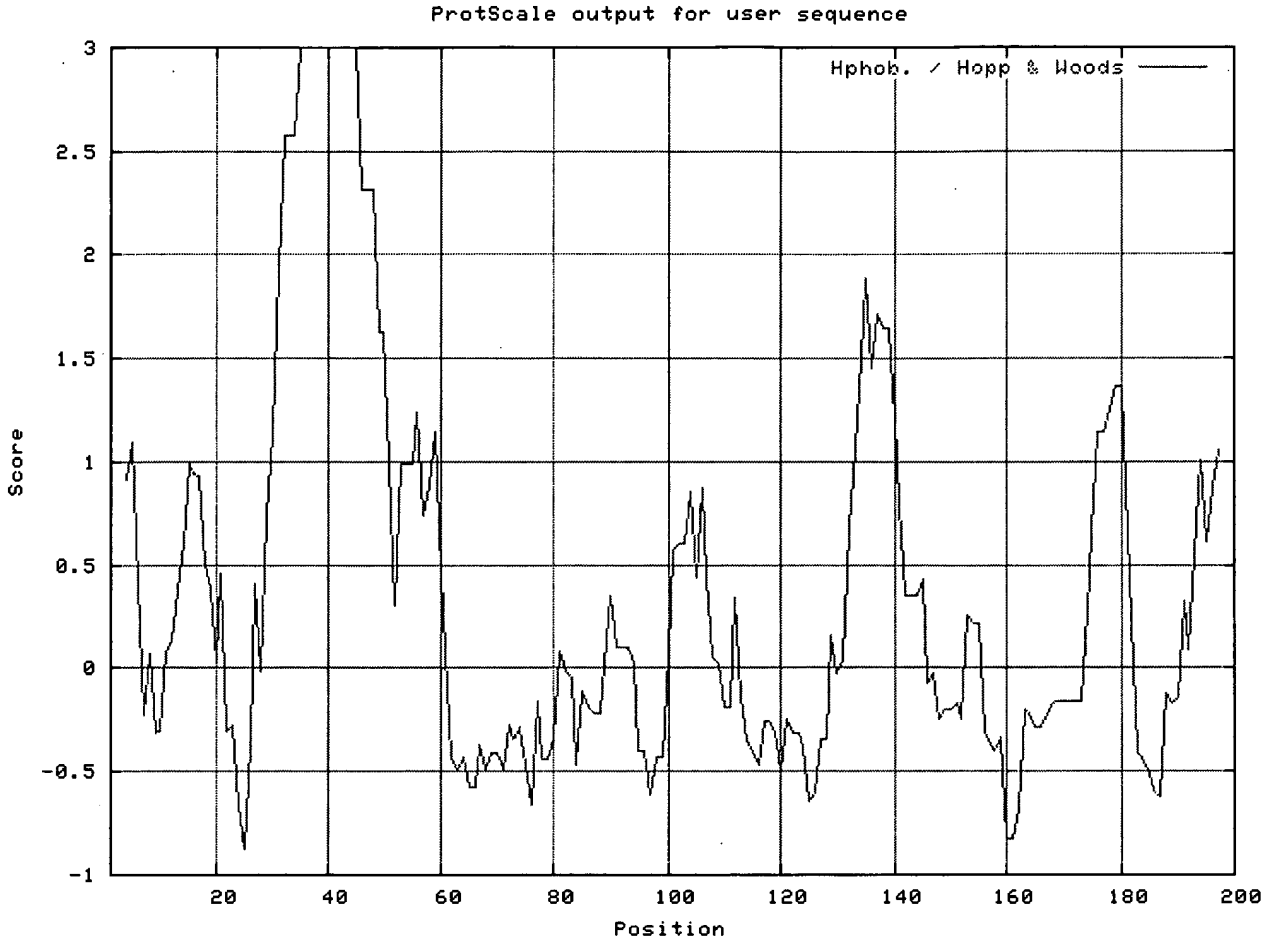
Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
   1     2     3     4     5     6     7
 1.00  1.00  1.00  1.00  1.00  1.00  1.00
 edge              center              edge
```

```
MIN: -0.871
MAX: 3.000
```



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ProtScale

User-provided sequence:

```
        10         20         30         40         50         60
VAPERQPSWD PSPVSSTVPA PSPLSAAAVS PSKLPEDDEP PARPPPPPPA SVSPQAEPVW
        70         80         90        100        110        120
TPPAPAPAAP PSTPAAPKRR GSSGAVVXXX XKIMDLKEQP GNTISAGQED FPSVLLETAA
       130        140        150        160        170        180
SXPSLSPLSA ASFKEHEYLG NLSTVLPTEG TLQENVSEAS KEVSEKAKTL LIDRDLTEFS
       190        200
ELEYSEMGSS FSVSPKAESA V
```

SEQUENCE LENGTH: 201

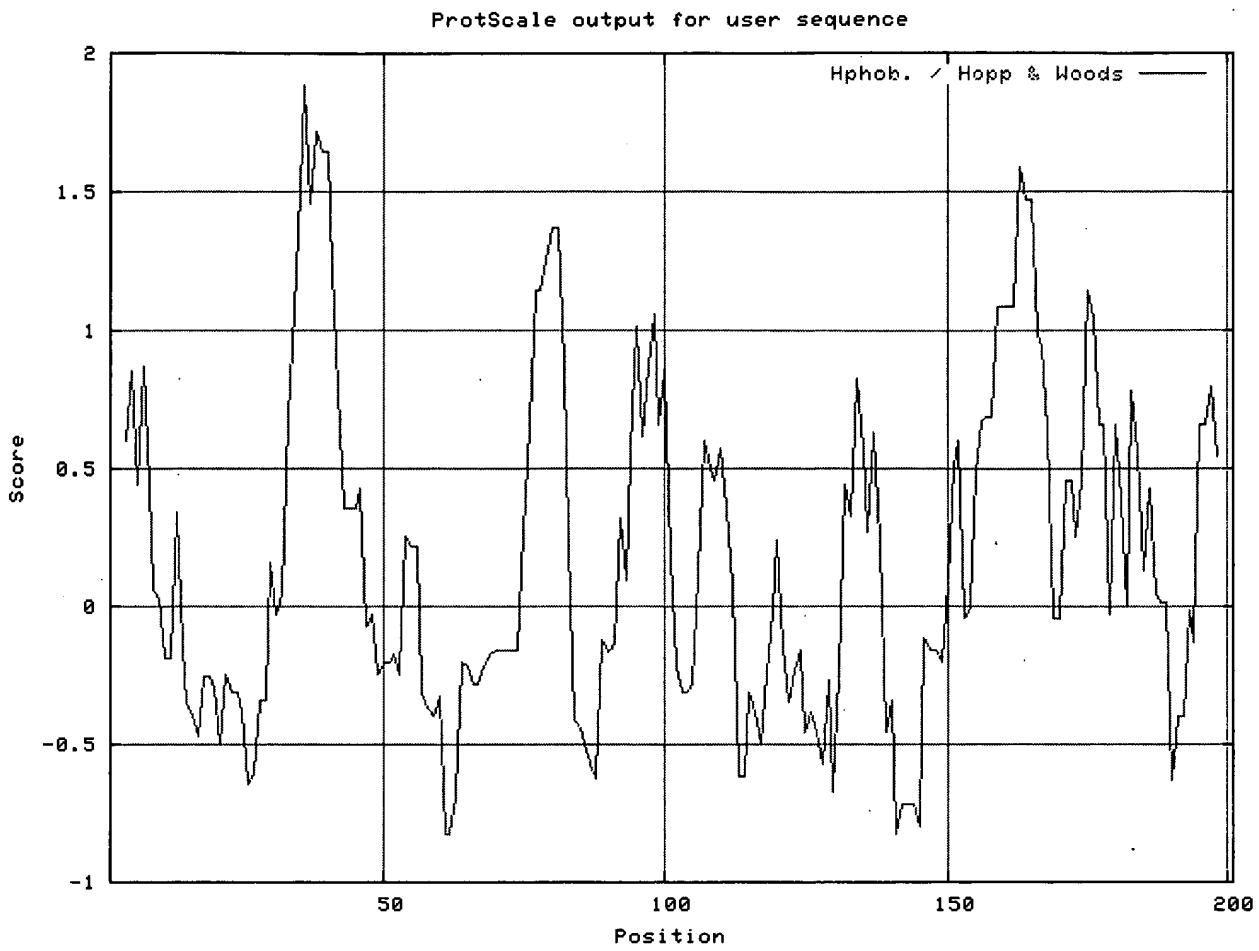
Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
   1     2     3     4     5     6     7
 1.00  1.00  1.00  1.00  1.00  1.00  1.00
 edge              center              edge
```

```
MIN: -0.829
MAX: 1.886
```



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ProtScale

User-provided sequence:

```
        10         20         30         40         50         60
TLQENVSEAS KEVSEKAKTL LIDRDLTEFS ELEYSEMGSS FSVSPKAESA VIVANPREEI
        70         80         90        100        110        120
IVKNKDEEEK LVSNNILHXQ QELPTALTKL VKEDEVVSSE KAKDSFNEKR VAVEAPMREE
       130        140        150        160        170        180
YADFKPFERV WEVKDSKEDS DMLAAGGKIE SNLESKVDKK CFADSLEQTN HEKDSESSND
       190        200
DTSFPSTPEG IKDRSGAYIT C
```

SEQUENCE LENGTH: 201

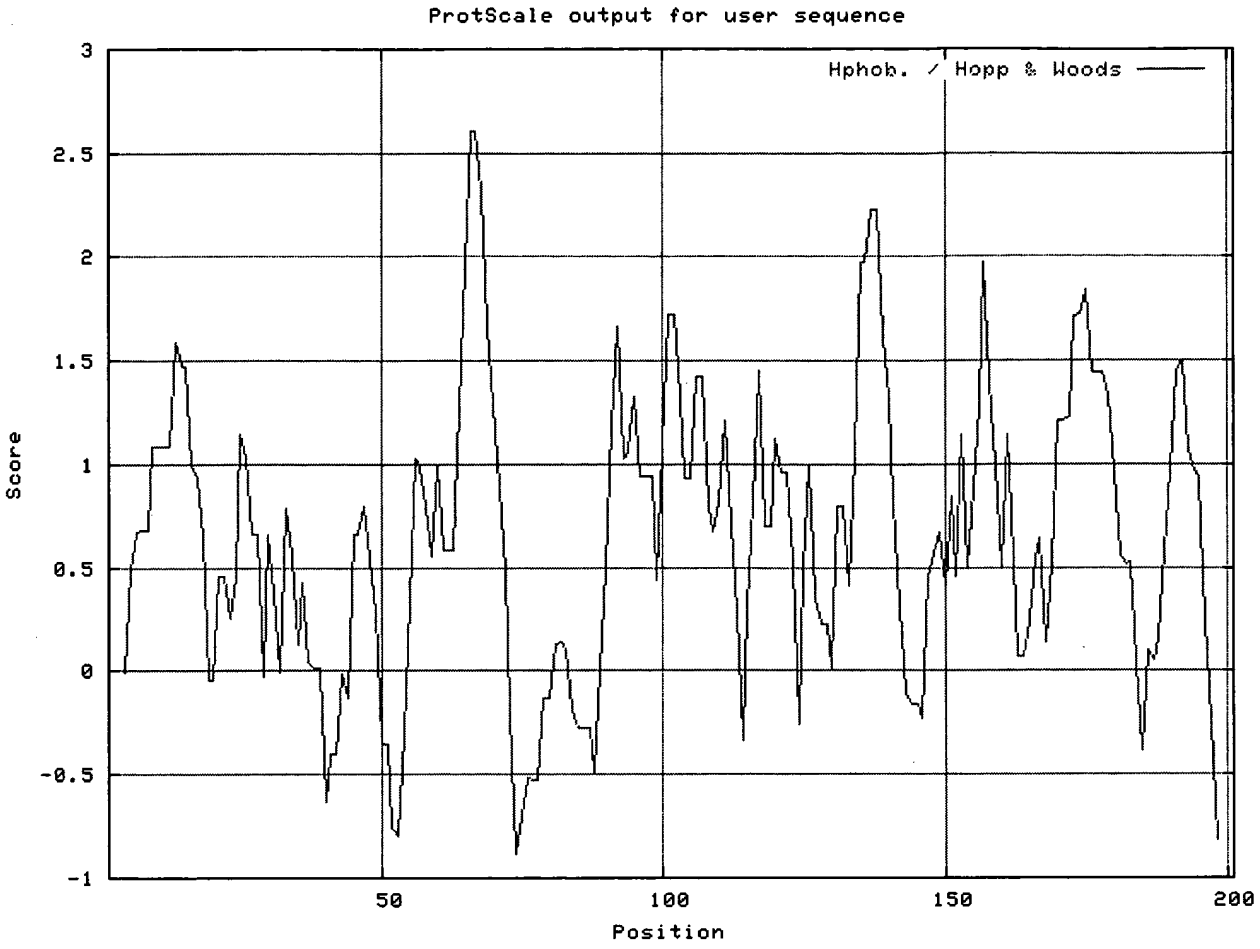
Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
   1     2     3     4     5     6     7
1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge              center              edge
```

```
MIN: -0.886
MAX: 2.600
```



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ProtScale

User-provided sequence:

```
        10         20         30         40         50
EVMQESLYPA AQLCPSFEES EATPSPVLPD IVMEAPLNSA VPSAGASVIQ
```

SEQUENCE LENGTH: 50

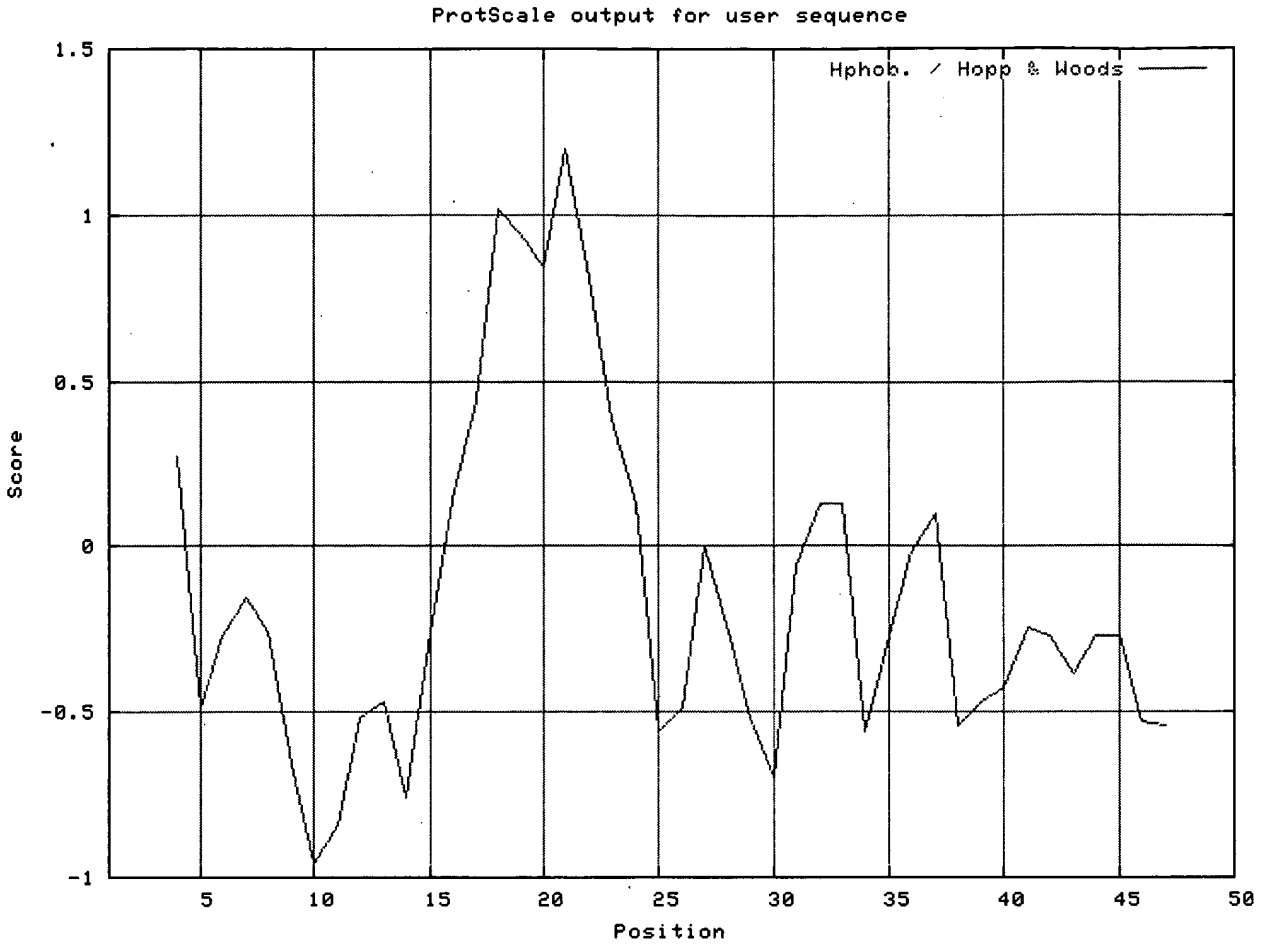
Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala:	-0.500	Arg:	3.000	Asn:	0.200	Asp:	3.000	Cys:	-1.000	Gln:	0.200
Glu:	3.000	Gly:	0.000	His:	-0.500	Ile:	-1.800	Leu:	-1.800	Lys:	3.000
Met:	-1.300	Phe:	-2.500	Pro:	0.000	Ser:	0.300	Thr:	-0.400	Trp:	-3.400
Tyr:	-2.300	Val:	-1.500	Asx:	1.600	Glx:	1.600	Xaa:	-0.215		

Weights for window positions 1,..,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -0.957
MAX: 1.200



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

ProtScale

User-provided sequence:

```
        10         20         30         40         50         60
RLSASPQELG KPYLESFQPN LHSTKDAASN DIPTLTKKEK ISLQMEEFNT AIYSNDDLLS
        70         80         90        100        110        120
SKEDKIKESE TFSDSSPIEI IDEFPTFVSA KDDSPKLAKE YTDLEVSDKS EIANIQSGAD
       130        140        150        160        170        180
SLPCLELPCD LSFKNIYPKD EVHVSDEFSE NRSSVSKASI SPSNVSALEP QTEMGSIVKS
       190        200        210        220        230        240
KSLTKEAEKK LPSDTEKEDR SLSAVLSAEL SKTSVVDLLY WRDIKKTGVV FGASLFLLLS
       250        260        270        280        290        300
LTVFSIVSVT AYIALALLSV TISFRIYKGV IQAIQKSDEG HPFRAYLESE VAISEELVQK
       310        320        330        340        350        360
YSNSALGHVN STIKELRRLF LVDDLVDSLK FAVLMWVFTY VGALFNGLTL LILALISLFS
       370        380        390        400
IPVIYERHQV QIDHYLGLAN KSVKDAMAKI QAKIPGLKRK AD
```

SEQUENCE LENGTH: 402

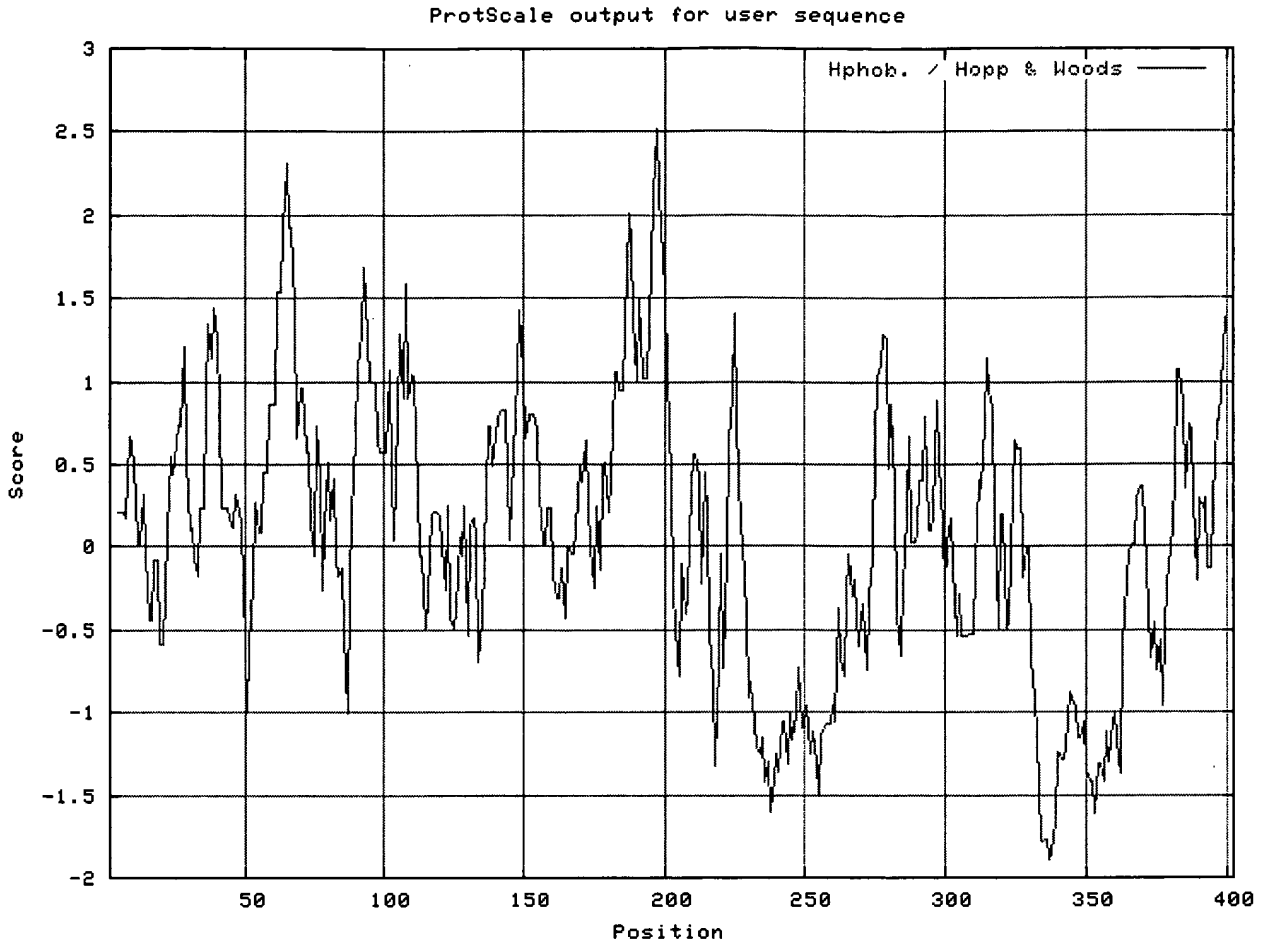
Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

```
Ala: -0.500  Arg:  3.000  Asn:  0.200  Asp:  3.000  Cys: -1.000  Gln:  0.200
Glu:  3.000  Gly:  0.000  His: -0.500  Ile: -1.800  Leu: -1.800  Lys:  3.000
Met: -1.300  Phe: -2.500  Pro:  0.000  Ser:  0.300  Thr: -0.400  Trp: -3.400
Tyr: -2.300  Val: -1.500  Asx:  1.600  Glx:  1.600  Xaa: -0.215
```

Weights for window positions 1,..,7, using **linear weight variation model**:

```
   1     2     3     4     5     6     7
 1.00  1.00  1.00  1.00  1.00  1.00  1.00
 edge              center              edge
```

```
MIN: -1.886
MAX: 2.514
```



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)